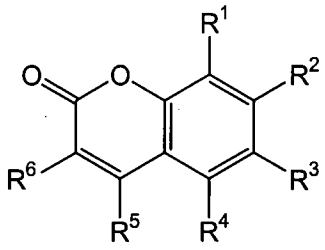
Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-83 (canceled)

84 (previously presented): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R^1, R^3, R^4 and R^6 are each H;

R^2 is -NHR^{15}; and

R^5 is -R^{14}-*SS*,

wherein:

R^{14} is –$CH_2C(O)NH$–;

R^{15} is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue; and

SS is a solid support.

85 (previously presented): The material in accordance with claim **84**, wherein R^{15} is an amine protecting group.

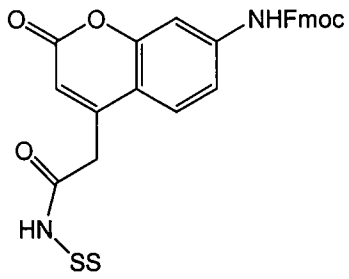
86 (previously presented): The material in accordance with claim **85**, wherein said amine protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

87 (previously presented): The material in accordance with claim **84**, wherein R^{15} is -C(O)-AA, wherein AA is an amino acid residue.

88 (previously presented): The material in accordance with claim **84**, wherein R^{15} is -C(O)-P, wherein P is a peptide sequence.

89 (previously presented): The material in accordance with claim **84**, wherein the solid support is a Rink resin.

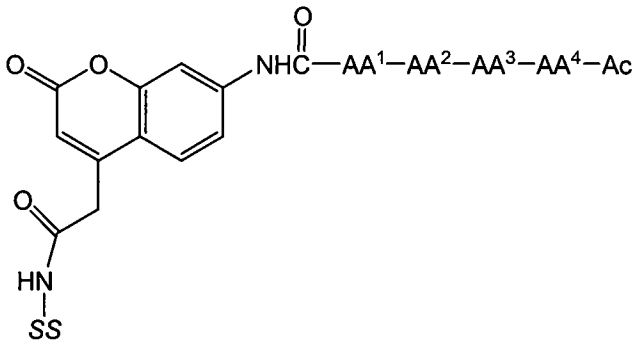
90 (previously presented): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

SS is a solid support, wherein said the support is a Rink resin.

91 (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

SS is a solid support, and

wherein:

for sub-library P1, each AA^1 is a different amino acid of the 20 amino acids, and each of AA^2-AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^2 is a different amino acid of the 20 amino acids, and each of AA^1, AA^3 and AA^4 is an isokinetic mixture of 20 amino acids;

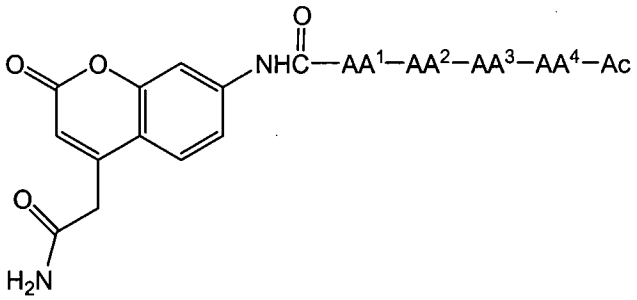
for sub-library P3, each of AA^3 is a different amino acid of the 20 amino acids, and each of AA^1, AA^2 and AA^4 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^4 is a different amino acid of the 20 amino acids, and each of AA^1, AA^2 and AA^4 is an isokinetic mixture of 20 amino acids.

92 (previously presented): The library in accordance with claim **91**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

93 (previously presented): The library in accordance with claim **91**, wherein the solid support is a Rink resin.

94 (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

for sub-library P1, each AA^1 is a different amino acid of the 20 amino acids, and each of AA^2-AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^2 is a different amino acid of the 20 amino acids, and each of AA^1, AA^3 and AA^4 is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA^3 is a different amino acid of the 20 amino acids, and each of AA^1, AA^2 and AA^4 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^4 is a different amino acid of the 20 amino acids, and each of AA^1, AA^2 and AA^4 is an isokinetic mixture of 20 amino acids.

95 (previously presented): The library in accordance with claim **94**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

96 (previously presented): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **91** or claim **94** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

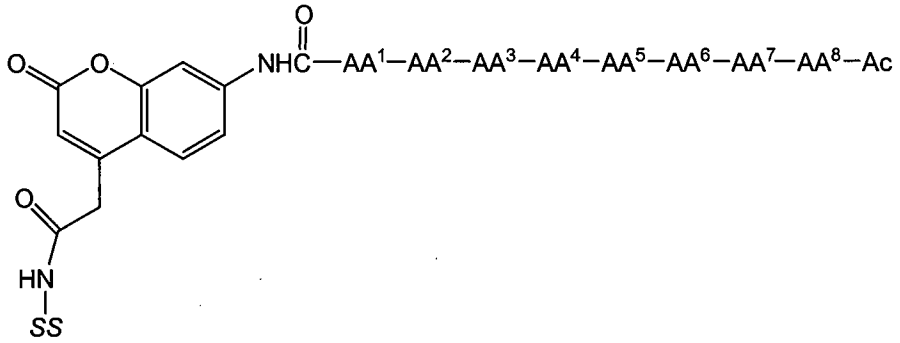
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

97 (previously presented): The method according to claim **96**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

98 (previously presented): The method according to claim **97**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

99 (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

SS is a solid support, and

wherein:

for each sub-library P1, P2, P3 and P4, AA^1, AA^2, AA^3 and AA^4 in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA^5 is a different amino acid of the 20 amino acids, and each of AA^6, AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^6 is a different amino acid of the 20 amino acids, and each of AA^5, AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

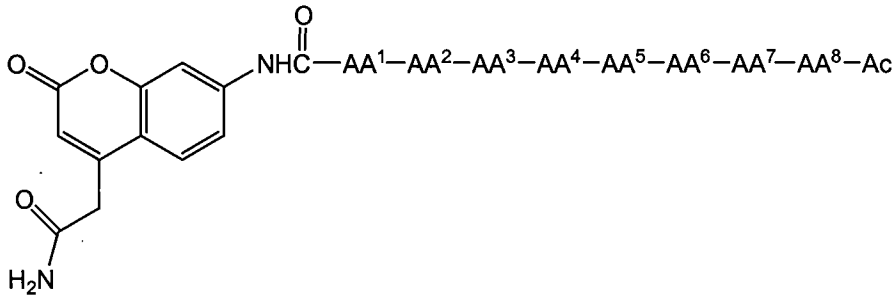
for sub-library P3, each of AA^7 is a different amino acid of the 20 amino acids, and each of AA^5, AA^6 and AA^8 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^8 is a different amino acid of the 20 amino acids, and each of AA^5, AA^6 and AA^7 is an isokinetic mixture of 20 amino acids.

100 (previously presented): The library in accordance with claim **99**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

101 (previously presented): The library in accordance with claim **99**, wherein the solid support is a Rink resin.

102 (previously presented): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

for each sub-library P1, P2, P3 and P4, AA^1, AA^2, AA^3 and AA^4 in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA^5 is a different amino acid of the 20 amino acids, and each of AA^6, AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA^6 is a different amino acid of the 20 amino acids, and each of AA^5, AA^7 and AA^8 is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA^7 is a different amino acid of the 20 amino acids, and each of AA^5, AA^6 and AA^8 is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA^8 is a different amino acid of the 20 amino acids, and each of AA^5, AA^6 and AA^7 is an isokinetic mixture of 20 amino acids.

103 (previously presented): The library in accordance with claim **102**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

104 (previously presented): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **99** or claim **102** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

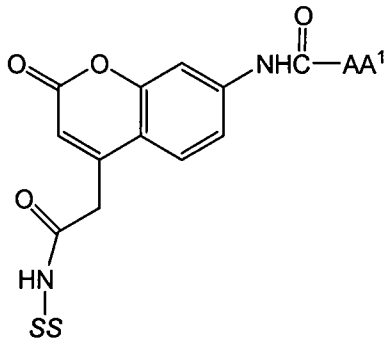
(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

105 (previously presented): The method according to claim **104**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

106 (previously presented): The method according to claim **105**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

107 (previously presented): A library of twenty fluorogenic amino acid amides having the structure:



wherein:

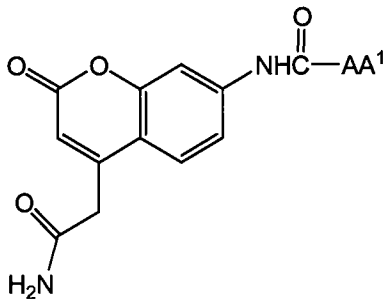
SS is a solid support, and

each AA^1 for the twenty fluorogenic amino acid amides is a different amino acid residue.

108 (previously presented): The library in accordance with claim **107**, wherein the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

109 (previously presented): The library in accordance with claim **108**, wherein the solid support is a Rink resin.

110 (previously presented): A library of twenty fluorogenic amino acids having the structure:



wherein:

each AA^1 for the twenty fluorogenic amino acids is a different amino acid residue

111 (previously presented): The library in accordance with claim **110**, wherein the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine..

112 (previously presented): A method of determining an amino acid specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of amino acids according to claim **108** or claim **110** in such a manner whereby the fluorogenic moiety is released from the amino acid, thereby forming a fluorescent moiety;

(b) detecting said fluorescent moiety;

(c) determining the identity of the amino acid, thereby determining said amino acid specificity profile of said protease.

113 (previously presented): The method according to claim **112**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

114 (previously presented): The method according to claim **113**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.